Original Research Article

Assessment of Genetic Variability and Character Association of Myanmar Local Rice (*Oryza sativa* L.) Germplasm

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ABSTRACT

Forty-two Myanmar local rice genotypes were evaluated to estimate the magnitude of genetic variability, relationship of some agronomic traits and genetic diversity. Randomized Complete Block (RCB) design with three replications was used to design this experiment at the Department of Plant Breeding, Physiology and Ecology, Yezin Agricultural University in Myanmar, 2017 (dry season). Genotypes showed highly significant difference for all the traits studied, meaning that the genotypes constitute a pool of germplasm with adequate genetic variability. Genetic variance was higher than environmental variance and heritability were above 80 % in all characters, which ensures the predominance of the genetic components among genotypes. The slight difference between genotypic coefficient variation (GCV) and phenotypic coefficient of variation (PCV) in all characters indicated there is enough genetic variability for the traits to be facilitated selection. High heritability with high genetic advance for spikelet panicle^{-1} and filled grain percent, their strong and positive correlation and the positive direct effect on yield plant^{-1} indicated that these are the importance indicator characters and their manipulation through selection. These characters can be utilized as selection criteria for further breeding programs related to high yielding rice varieties.

Keywords: correlation, genetic advance, heritability, path analysis and variability

1. INTRODUCTION

The success of increasing the productivity of any crop through breeding largely depends on the presence of variability among the breeding materials (1, 2). Genetic variability can provides a different kinds of genotypes that could be selected to develop new improved varieties (3). It is necessary to estimate heritability to make a plan of an efficient breeding programme (4). Knowledge about heritability can help plant breeders to predict the genetic nature of the succeeding generation, to do an effective selection and to attain genetic improvement through selection (5).

Yield is a complex character and highly influenced by the environment. The direct selection for yield alone limits the selection efficiency for the improvement of cultivars. Therefore, indirect selection for yield components could be achieved higher yield (6). The correlation coefficients provide information about interrelationship among yield and its components. This information is very helpful for the development of efficient selection strategy (7). Correlation does not generally imply causation; however, the path analysis can applied cause and effect of the related traits. Its application, however, is not limited to agriculture. Several authors have discussed the use of path analysis in epidemiology (8-12) and in sociology (13-16).

Consequently, the contribution of each character to yield through path analysis could be estimated for picking up appropriate traits for indirect selection.

Therefore, path coefficient analysis is essential to gather information for optimum combination of yield contributing characters and to know the implication of the interrelationships of various characters in a single genotype (17). Knowledge based on direct and indirect effect between grain yield and other characters can be helpful to plant breeder in efficient selection of suitable cultivars of rice. Therefore, this study was conducted to estimate the magnitude of genetic variability and relationship of some agronomic attributes of Myanmar local rice genotypes.

2. MATERIAL AND METHODS

Forty-two Myanmar local rice genotypes were grown in Randomized Complete Block design with three replications at the field of the Department of Plant Breeding, Physiology and Ecology, Yezin Agricultural University, Nay Pyi Taw, Myanmar, in 2017 dry season (Appendix 1). The spacing was 20 cm x 20cm and one seedling per hill was planted. The data were collected on five randomly chosen plants from each genotype per replication for agronomical traits. To obtain optimum performance, recommended cultural practices was followed whenever needed. The data on days to flowering (days), plant height (cm), effective tillers hill^{-1} (no.), panicle/straw weight ratio, panicle length (cm), filled grain percent, spikelet panicle^{-1} (no.), 1000 grain weight (g), harvest index, yield plant^{-1} (g) were collected according to the Standard Evaluation System for Rice (18) released by International Rice Research Institute (IRRI), Philippines. Analysis of variance (ANOVA) was carried out on the data to assess the genotypic effects for RCB design in STAR (Statistical Tool for Agricultural Research, version 2.0.1) (19). Estimates of variance components were generated based on mean squares values. Broad-sense heritability (H) was calculated as the ratio of the genotypic variance to the phenotypic variance using the formula according to (20). Genetic advance was calculated at 10% selection intensity (i=1.76). Phenotypic and genotypic coefficients of correlation (PCV and GCV) and path analysis were computed using SPAR 2 software.

3. RESULT AND DISCUSSION

3.1 Analysis of Variance (ANOVA) for agronomic traits of 42 Myanmar local rice genotypes

The mean square values due to genotypes were highly significant differences in days to flowering, plant height, effective tillers hill^{-1}, panicle/ straw ratio, panicle length, filled grain percent, spikelet panicle^{-1}, 1000 grain weight, harvest index and yield plant^{-1} (Table 1). This result indicated that there was the high genetic variability within the genotypes and hence it would be beneficial for the improvement of the crop.

Table 1. Analysis of variance on agronomic traits of 42 local rice genotypes

Source of variation	**Mean Squares**			**Coefficient of Variation (CV)**
	Replication	**Genotypes**	**Error**	
Days to flowering	13.883	496.163**	4.309	2.04
Plant height	4.661	1180.330**	9.377	2.40
Effective tillers hill^{-1}	0.372	36.129**	1.901	10.55

Panicle/Straw weight ratio	0.003	0.246**	0.003	14.31
Panicle length	3.369	22.613**	2.437	6.76
Filled grain percent	158.030	1222.443**	44.659	11.10
Spikelets panicle^{-1}	474.289	2472.382**	173.790	15.35
1000 grains weight	1.211	43.433**	0.452	2.74
Harvest Index	0.0001	0.061**	0.0006	9.77
Yield plant^{-1}	20.047	415.924**	8.321	15.72

Significant at *$P < 0.05$; ** $P < 0.01$*

3.2 Genetic Variability occurred in 42 genotypes of Myanmar local rice

Genetic parameters of 42 genotypes of Myanmar local rice are presented in Table 2. The results revealed a wide range of variability among all tested genotypes for effective tillers hill^{-1}, panicle/straw weight ratio, harvest index, filled grain percent, spikelet panicle^{-1} and yield plant^{-1}. The values of phenotypic variance (V_P) were higher than that of genotypic variance (V_G) in all traits. There is neglected amount of V_E in all traits, meaning that the variation occurred in all genotypes is found to be due to genetic effect rather than environmental effect.

In all traits, the phenotypic coefficient of variation (PCV) was also higher than genotypic coefficient of variation (GCV). The highest PCV and GCV were recorded for the trait of panicle/straw weight ratio (75.81%, 75.36%) followed by yield plant^{-1} (64.17%, 63.52%). In contrast, the lowest PCV and GCV belonged to the traits of panicle length (11.89%, 11.23%) followed by days to flowering (12.64%, 12.58%). It could be sure that all the traits in this study were mainly affected by genes and less affected by environment. This finding was the same with the result occurred by (21), (22), (23, 24). Therefore, selection on the basis of phenotype alone could be effective for the improvement of these traits. The slight difference between genotypic and phenotypic coefficients of variation (GCV and PCV) was observed in all traits revealed the presence of sufficient genetic variability for the traits which may facilitate effective selection.

High broad sense heritability (H) was found for all traits with the range from 89.22% to 99.21%. The values of heritability over 99% were recorded for the traits of harvest index (99.02%), days to flowering (99.13%) and plant height (99.21%). It could be suggested that these traits would highly respond to selection due to the presence of high genetic variability and heritability. High genetic advance was observed in spikelet panicle^{-1} (46.97), plant height (34.63), filled grain percent (34. 23) and days to flowering (22.44). Moderate genetic variance was found to be in yield plant^{-1} (20.31). Low genetic advance was found in harvest index (0.25), panicle/straw weight ratio (0.50), panicle length (4.31), effective tillers hill^{-1} (5.79) and 1000 grain weight (6.63).
Occurrence of high heritability with high genetic advance for spikelet panicle^{-1}, plant height, filled grain percent and days to flowering indicated that additive gene action is controlling these traits. This pointed out that the less effect of environment in the expression of these traits and it can be amenable for simple selection. The traits with high heritability and moderate genetic advance found in yield plant^{-1} and it could be governed by both additive and non-additive gene actions.

Table 2. Genetic parameters for yield and its component traits in 42 different local rice genotypes.

Traits	**Mean**	**V_G**	**V_P**	**V_E**	**GCV (%)**	**PCV (%)**	**H (%)**	**GA (%)**
Days to flowering (day)	101.76	163.95	165.39	1.44	12.58	12.64	99.13	22.44
Plant Height (cm)	127.63	390.32	393.44	3.13	15.48	15.54	99.21	34.63
Effective tillers hill^{-1} (no.)	13.07	11.41	12.04	0.63	25.84	26.55	94.74	5.79
Panicle/Straw weight ratio	0.38	0.0811	0.0821	0.0010	75.36	75.81	98.82	0.50
Harvest Index	0.25	0.0203	0.0205	0.0002	58.08	58.37	99.02	0.25
Panicle Length (cm)	23.09	6.73	7.54	0.81	11.23	11.89	89.22	4.31
Filled grain percent (%)	60.19	392.59	407.48	14.89	32.92	33.54	96.35	34.23
Spikelet panicle^{-1} (no.)	85.89	766.20	824.13	57.93	32.23	33.42	92.97	46.97
1000 grains weight (g)	24.55	14.33	14.48	0.15	15.42	15.50	98.96	6.63
Yield plant^{-1} (g)	18.35	135.87	138.64	2.77	63.52	64.17	98.00	20.31

V_G= Genotypic variance, V_P=Phenotypic variance, GCV= Genotypic Coefficient of Variation, PCV= Phenotypic Coefficient of Variation, H= Heritability in broad sense, GA=Genetic advance

3.3 Genotypic and Phenotypic Correlations among traits

The relatedness of yield and its components traits can be identified by correlation analysis. It is important in indirect selection for higher yield improvement. The phenotypic and genotypic correlations for yield and its component traits are presented in Table 3. There was a significant and positive genotypic and phenotypic correlation of yield plant^{-1} with effective tillers hill^{-1} and panicle/straw ratio, harvest index, filled grain percent and spikelet panicle^{-1}. Therefore, this could be highlighted that these traits are major factors for improving grain yield. In addition, direct selection towards these characters would be effective for ensuring high grain yield in rice. These results collaborate with the finding of (25) who observed a positive and significant correlation between grain yield and number of panicle/m^2, (26) for the number of panicles per plant and (27) for spikelet panicle^{-1}. Conversely, grain yield exhibited negative correlation with days to flowering, panicle length and 1000 grain weight, but not significant. Therefore, grain yield could be improved by selecting early flowering genotypes.

Table 3. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficient among 10 quantitative traits of Myanmar local rice genotypes

	DTF	**PHt**	**EffT**	**PSR**	**HI**	**PLen**	**FGP**	**SPP**	**TGW**	**YPP**
DTF		0.340*	-0.149	-0.229	-0.278	0.234	-0.356*	0.022	-0.091	-0.126

PHt	0.347*		-0.297	-0.440**	-0.38*	0.456**	-0.298	-0.112	0.498**	-0.204
EffT	-0.176	-0.337		0.740**	0.759**	-0.175	0.566**	0.426**	-0.335*	0.748**
PSR	-0.233	-0.456**	0.675**		0.982**	-0.178	0.679**	0.640**	-0.164	0.820**
HI	-0.284	-0.392*	0.693**	0.983**		-0.171	0.734**	0.685**	-0.144	0.857**
PLen	0.279	0.520**	-0.141	-0.229	-0.215		-0.295	0.068	0.207	-0.068
FGP	-0.384*	-0.320*	0.667**	0.718**	0.775**	-0.335*		0.499**	-0.203	0.805**
SPP	0.035	-0.111	0.599**	0.718**	0.767**	0.048	0.600		-0.161	0.802**
TGWt	-0.100	0.511	-0.356*	-0.167	-0.146	0.248	-0.218	-0.184		-0.168
YPP	-0.136	-0.212	0.819**	0.853**	0.891**	-0.092	0.846**	0.853**	-0.182	

DTF = Days to flowering, PHt = Plant Height, EffT = Effective tillers hill^{-1}, PSR = Panicle/Straw weight ratio, HI = Harvest Index, PLen = Panicle Length, FGP = Filled grain percent, SPP = Spikelet panicle^{-1}, TGWt = 1000 grains weight, YPP = Yield plant^{-1}
Significant at *$* P < 0.05$; $** P < 0.01$*

3.4 Path analysis

Path analysis allows separating the direct effect and their indirect effects through other attributes by apportioning the correlations for better interpretation of cause and effect (7). Path analysis has been conducted taking grain yield per plant as dependent variable. Effective tiller plant^{-1} had highest direct effect on yield plant^{-1} followed by filled grain percent, spikelet panicle^{-1} (Table 4). These characters had also positive and highly significant correlation with yield plant^{-1}. This indicated that the correlation revealed the true relationship and direct selection of these characters is likely to be effective in increasing yield plant^{-1}. Results on importance of direct effect of effective tiller plant^{-1} were reported by several researchers (28-32). The spikelet panicle^{-1} had positive direct effect on the yield plant^{-1} was also reported by (33-40).

Panicle/straw weight ratio and panicle length has high indirect effect via effective tillers hill^{-1} and filled grain percent. Filled grain percent and spikelet panicle^{-1} were also highly contributed indirectly via effective tillers hill^{-1}. These indirect effects had not only supported the low magnitude direct effect but also resulted in high significant positive correlation with grain yield. Panicle/straw weight ratio exhibited high negative direct effects on yield plant^{-1}. Similar finding was reported by (41) for effective tillers plant^{-1}.

The residual effect determines how best the causal factors account for the variability of the dependent factor such as standard evaluation score. The residual effect was 0.1676 at genotypic level. This indicated that the characters which are selected in this study contributed 84% of variability.

Table 4. Path coefficient analysis showing direct and indirect effects of various traits on yield plant^{-1} in Myanmar local rice genotype

	DTF	PHt	EffT	PSR	HI	PLen	FGP	SPP	TGW	r_g with YLD
DTF	**0.0501**	0.0174	-	-	0.014	-0.0088	-	0.0017	-0.005	-0.136

			0.0117	0.0142			0.0192			
PHt	0.0223	**0.0643**	-0.0293	-0.0252	0.0335	-0.0217	-0.0206	-0.0071	0.0329	-0.212
EffT	-0.1225	-0.2392	**0.5247**	0.5159	-0.1202	0.3885	0.3768	0.3766	-0.0876	0.819**
PSR	0.1171	0.1618	-0.4053	**-0.4122**	0.0886	-0.3129	-0.3194	-0.3163	0.0603	0.853**
HI	0.0165	0.0307	-0.0135	-0.0127	**0.059**	-0.0103	-0.0198	0.0028	0.0146	0.891**
PLen	-0.0511	-0.098	0.2152	0.2206	-0.051	**0.2906**	0.1938	0.174	-0.1034	-0.092
FGP	-0.1736	-0.1446	0.3246	0.3502	-0.1514	0.3015	**0.452**	0.271	-0.0984	0.846**
SPP	0.0127	-0.0403	0.2606	0.2786	0.0173	0.2174	0.2177	**0.3632**	-0.0669	0.853**
TGWt	-0.0071	0.0364	-0.0119	-0.0104	0.0177	-0.0254	-0.0155	-0.0131	**0.0713**	-0.182

Note: Diagonal values are direct effects, Residual effect = 0.1676, Significant at *$* P < 0.05$; $** P < 0.01$*.

DTF = Days to flowering, PHt = Plant Height, EffT = Effective tillers hill^{-1}, PSR = Panicle/Straw weight ratio, HI = Harvest Index, PLen = Panicle Length, FGP = Filled grain percent, SPP = Spikelet panicle^{-1}, TGWt = 1000 grains weight, YPP = Yield plant^{-1}

4. CONCLUSION

The agronomic performance of the rice genotypes showed the highly significant differences among the genotypes in respect to all the traits. This indicates that the genotypes tested in this study contained adequate genetic variability for breeding purpose. Genetic variance was higher than environmental variance and heritability were higher than 80 % for all traits, ensuring the predominance of the genetic components among genotypes. The slight difference between genotypic and phenotypic coefficients of variation (GCV and PCV) in all characters was found to be the presence of sufficient genetic variability for the traits which may facilitate selection. High heritability with high genetic advance for spikelet panicle^{-1} and filled grain percent, their strong and positive correlation and the positive direct effect on yield plant^{-1} indicated that these are the importance indicator characters and their manipulation through selection. These characters can be utilized as selection criteria for further breeding programs related to high yielding rice varieties.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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APPENDIX 1. List of local rice genotypes used for this study

No.	Germplasm	Source	No.	Germplasm	Source
1	BaKauk	DaWai, YAU collection	22	LawThawGyi	DAR, Seed Bank
2	BayKyaung	DAR, Seed Bank	23	LetYoneGyi	DAR, Seed Bank
3	GaukRa	DAR, Seed Bank	24	LetYwesin	DAR, Seed Bank
4	KalarGyi	Mon, YAU collection	25	LopaZa	DAR, Seed Bank
5	KalarLay	DAR, Seed Bank	26	MaeKhalar-5	DAR, Seed Bank

6	KuTaungMyoTun	DAR, Seed Bank	27	MaungPhaLo	DAR, Seed Bank
7	KhaingShweWar	Myeik, YAU collection	28	MuyinSaba	DAR, Seed Bank
8	KhaoHline	DAR, Seed Bank	29	PaDinThuMa	DAR, Seed Bank
9	KhaoLai	DAR, Seed Bank	30	PhoKawGyi	DAR, Seed Bank
10	KhaoLamil	DAR, Seed Bank	31	PyawtTun	YAU collection
11	KhaoLan	DAR, Seed Bank	32	SeinGyi	DAR, Seed Bank
12	KhaoLin	DAR, Seed Bank	33	ShweHinThar	DAR, Seed Bank
13	KhaoLiPaw	DAR, Seed Bank	34	ShweYinAye	Shan, YAU collection
14	KhaoMaPhut	DAR, Seed Bank	35	TaTaungPo	DAR, Seed Bank
15	KhaoNyoHon	DAR, Seed Bank	36	TaungAtBeSaba	DAR, Seed Bank
16	KhaoPhaLin	DAR, Seed Bank	37	TaungHtakePan	Bago, YAU collection
17	KhaoPiPaung	DAR, Seed Bank	38	TaungYarSaba	DAR, Seed Bank
18	KhaoTan	DAR, Seed Bank	39	TinTayar	YAU collection
19	KhaowaA	DAR, Seed Bank	40	WetSiPhyu	DAR, Seed Bank
20	KunLone	DAR, Seed Bank	41	YarPyae	YAU collection
21	KyweChaeManaing	DAR, Seed Bank	42	YawShweWar	DaWai, YAU collection